SEQUENCE LISTING

<110> Thayer, Edward C.
      Webster, Philippa J.

<120> Human Secreted Protein, Zzp1

<130> 00-54

<150> 60/222,814
<151> 2000-08-04

<150> 60/260,512
<151> 2001-01-09

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ctg ctg gtt gcc acc ctg ggg ctg ggt agg tgg ctc cag ccc gac cca   96
Leu Leu Val Ala Thr Leu Gly Leu Gly Arg Trp Leu Gln Pro Asp Pro
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ggc ctc cgg cac agc tac gac tgt ggg atc aag gga atg cag ctg ctg   144
Gly Leu Arg His Ser Tyr Asp Cys Gly Ile Lys Gly Met Gln Leu Leu
        35   40   45

gtg ttc ccc agg cca ggc cag act ctc cgc ttc aag gtg gtg gat gaa   192
Val Phe Pro Arg Pro Gly Gln Thr Leu Arg Phe Lys Val Val Asp Glu
      50   55   60

ttt ggg aac cga ttt gat gtc aac aac tgc tcc atc tgc tac cac tgg   240
Phe Gly Asn Arg Phe Asp Val Asn Asn Cys Ser Ile Cys Tyr His Trp
      65   70   75   80

gtc acc tcc agg ccg cag gag cct gca gtc ttc tcg gcc gat tac aga   288
Val Thr Ser Arg Pro Gln Glu Pro Ala Val Phe Ser Ala Asp Tyr Arg
                  85   90   95

ggc tgc cac gtg ctg gag aag gat ggg cgt ttc cac ctg agg gtg ttc   336
Gly Cys His Val Leu Glu Lys Asp Gly Arg Phe His Leu Arg Val Phe
            100   105   110

atg gag gct gtg ctg ccc aat ggt cgt gtg gat gtg gca caa gac gct   384
Met Glu Ala Val Leu Pro Asn Gly Arg Val Asp Val Ala Gln Asp Ala
            115   120   125

act ctg atc tgt ccc aaa cct gac ccc tcc cgg act ctg gac tcc cag   432
Thr Leu Ile Cys Pro Lys Pro Asp Pro Ser Arg Thr Leu Asp Ser Gln
            130   135   140

ctg gca cca ccc gcc atg ttc tct gtc tca acc cca caa acc ctt tcc   480
Leu Ala Pro Pro Ala Met Phe Ser Val Ser Thr Pro Gln Thr Leu Ser
145   150   155   160

ttc ctc ccc acc tct ggc cat acc tcc caa ggc tct ggc cat gcc ttt   528
Phe Leu Pro Thr Ser Gly His Thr Ser Gln Gly Ser Gly His Ala Phe
               165   170   175

ccc agc cca ctg gac cca ggg cac agc tct gtc cac cca acc cct gct   576
Pro Ser Pro Leu Asp Pro Gly His Ser Ser Val His Pro Thr Pro Ala
            180   185   190

tta cca tcc cct gga cct gga cct acc ctc gcc acc ctg gct caa ccc   624
Leu Pro Ser Pro Gly Pro Gly Pro Thr Leu Ala Thr Leu Ala Gln Pro
            195   200   205

cac tgg ggc acc ttg gaa cac tgg gat gtg aac aaa cga gat tac ata   672
His Trp Gly Thr Leu Glu His Trp Asp Val Asn Lys Arg Asp Tyr Ile
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Gly Thr His Leu Ser Gln Glu Gln Cys Gln Val Ala Ser Gly His Leu
225             230             235             240

ccc tgc atc gtg aga aga act tca aaa gaa gcc tgt cag cag gct ggc     768
Pro Cys Ile Val Arg Arg Thr Ser Lys Glu Ala Cys Gln Gln Ala Gly
            245             250             255

tgc tgc tat gac aac acc aga gag gtt ccc tgt tac tat ggc aac aca     816
Cys Cys Tyr Asp Asn Thr Arg Glu Val Pro Cys Tyr Tyr Gly Asn Thr
            260             265             270

gct act gtc cag tgc ttc aga gat ggc tac ttc gtc ctc gta gtg tcc     864
Ala Thr Val Gln Cys Phe Arg Asp Gly Tyr Phe Val Leu Val Val Ser
            275             280             285

caa gaa atg gcc ttg aca cac agg atc aca ctg gcc aac atc cac ctg     912
Gln Glu Met Ala Leu Thr His Arg Ile Thr Leu Ala Asn Ile His Leu
        290             295             300

gcc tat gcc ccc acc agc tgc tcc cca aca cag cac acg gaa gct ttc     960
Ala Tyr Ala Pro Thr Ser Cys Ser Pro Thr Gln His Thr Glu Ala Phe
305             310             315             320

gtg gtc ttc tac ttc cct ctc acc cac tgt gga acc aca atg cag gtg    1008
Val Val Phe Tyr Phe Pro Leu Thr His Cys Gly Thr Thr Met Gln Val
                325             330             335

gct ggc gac cag ctc atc tat gag aac tgg ctg gtg tct ggc atc cac    1056
Ala Gly Asp Gln Leu Ile Tyr Glu Asn Trp Leu Val Ser Gly Ile His
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atc caa aag ggg cca cag ggt tcc atc acg cgg gac agc acc ttc cag    1104
Ile Gln Lys Gly Pro Gln Gly Ser Ile Thr Arg Asp Ser Thr Phe Gln
            355             360             365

ctt cat gtg cgc tgt gtc ttc aac gcc agt gac ttc ctg ccc att cag    1152
Leu His Val Arg Cys Val Phe Asn Ala Ser Asp Phe Leu Pro Ile Gln
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gca tcc att ttc cca ccc cca tcg cct gct cct atg acc cag ccc ggc    1200
Ala Ser Ile Phe Pro Pro Pro Ser Pro Ala Pro Met Thr Gln Pro Gly
385             390             395             400


ccc ctg cgg ctt gag ctg cgg att gcc aaa gac gag acc tgc agc tcg    1248
Pro Leu Arg Leu Glu Leu Arg Ile Ala Lys Asp Glu Thr Cys Ser Ser
            405             410             415


tac tat ggg gag gat gac tat ccc atc gtg agg ctg ctc cga gaa cca    1296
Tyr Tyr Gly Glu Asp Asp Tyr Pro Ile Val Arg Leu Leu Arg Glu Pro
            420             425             430


gtc cat gtg gag gtc cgg ctt ctg cag agg aca gac ccc aac ctg gtc    1344
Val His Val Glu Val Arg Leu Leu Gln Arg Thr Asp Pro Asn Leu Val
            435             440             445


ctg ctg ctg cac cag tgc tgg ggc gct ccc agt gcc aac ccc ttc cag    1392
Leu Leu Leu His Gln Cys Trp Gly Ala Pro Ser Ala Asn Pro Phe Gln
    450             455             460


cag ccc cag tgg ccc atc ctg tca gac ggc tgc cct ttc aag ggc gac    1440
Gln Pro Gln Trp Pro Ile Leu Ser Asp Gly Cys Pro Phe Lys Gly Asp
465             470             475             480


agc tac aga acc caa atg gta gcc ttg gac ggg gcc aca cct ttc cag    1488
Ser Tyr Arg Thr Gln Met Val Ala Leu Asp Gly Ala Thr Pro Phe Gln
                485             490             495


tcg cac tac cag cga ttc act gtt gct acc ttc gcc ctc ctg gac tca    1536
Ser His Tyr Gln Arg Phe Thr Val Ala Thr Phe Ala Leu Leu Asp Ser
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ggc tcc cag aga gcc ctc aga gga ctg gtt tac ttg ttc tgc agc acc    1584
Gly Ser Gln Arg Ala Leu Arg Gly Leu Val Tyr Leu Phe Cys Ser Thr
            515             520             525


tct gcc tgc cac acc tca ggg ctg gag act tgc tcc act gca tgt agc    1632
Ser Ala Cys His Thr Ser Gly Leu Glu Thr Cys Ser Thr Ala Cys Ser
    530             535             540


act ggc act aca aga cag cga cga tcc tca ggt cac cgt aat gac act    1680
Thr Gly Thr Thr Arg Gln Arg Arg Ser Ser Gly His Arg Asn Asp Thr
545             550             555             560
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gcc agg ccc cag gac atc gtg agc tct ccg ggg cca gtg ggc ttt gag    1728
Ala Arg Pro Gln Asp Ile Val Ser Ser Pro Gly Pro Val Gly Phe Glu
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gat tct tat ggg cag gag ccc aca ctt ggg ccc aca gac tcc aat ggg    1776
Asp Ser Tyr Gly Gln Glu Pro Thr Leu Gly Pro Thr Asp Ser Asn Gly
                580                 585                 590

aac tcc agc ctg aga cct ctc ctt tgg gcg gtc ctt ttg ctg cca gct    1824
Asn Ser Ser Leu Arg Pro Leu Leu Trp Ala Val Leu Leu Leu Pro Ala
                595                 600                 605

gtt gcc ctg gtc ctt ggg ttt ggt gtc ttt gtg ggc ctg agc cag acc    1872
Val Ala Leu Val Leu Gly Phe Gly Val Phe Val Gly Leu Ser Gln Thr
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tgg gcc cag aag ctc tgg gaa agc aac aga cag tga                    1908
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Gly Leu Arg His Ser Tyr Asp Cys Gly Ile Lys Gly Met Gln Leu Leu
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Val Phe Pro Arg Pro Gly Gln Thr Leu Arg Phe Lys Val Val Asp Glu
    50                  55                  60
Phe Gly Asn Arg Phe Asp Val Asn Asn Cys Ser Ile Cys Tyr His Trp
65                  70                  75                  80
Val Thr Ser Arg Pro Gln Glu Pro Ala Val Phe Ser Ala Asp Tyr Arg
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Gly Cys His Val Leu Glu Lys Asp Gly Arg Phe His Leu Arg Val Phe
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Met Glu Ala Val Leu Pro Asn Gly Arg Val Asp Val Ala Gln Asp Ala
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Thr Leu Ile Cys Pro Lys Pro Asp Pro Ser Arg Thr Leu Asp Ser Gln
    130                 135                 140
Leu Ala Pro Pro Ala Met Phe Ser Val Ser Thr Pro Gln Thr Leu Ser
145                 150                 155                 160
Phe Leu Pro Thr Ser Gly His Thr Ser Gln Gly Ser Gly His Ala Phe
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Pro Ser Pro Leu Asp Pro Gly His Ser Ser Val His Pro Thr Pro Ala
                180                 185                 190
Leu Pro Ser Pro Gly Pro Gly Pro Thr Leu Ala Thr Leu Ala Gln Pro
                195                 200                 205
His Trp Gly Thr Leu Glu His Trp Asp Val Asn Lys Arg Asp Tyr Ile
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Gly Thr His Leu Ser Gln Glu Gln Cys Gln Val Ala Ser Gly His Leu
225                 230                 235                 240
Pro Cys Ile Val Arg Arg Thr Ser Lys Glu Ala Cys Gln Gln Ala Gly
                245                 250                 255
Cys Cys Tyr Asp Asn Thr Arg Glu Val Pro Cys Tyr Tyr Gly Asn Thr
                260                 265                 270
Ala Thr Val Gln Cys Phe Arg Asp Gly Tyr Phe Val Leu Val Val Ser
    275                 280                 285
Gln Glu Met Ala Leu Thr His Arg Ile Thr Leu Ala Asn Ile His Leu
    290                 295                 300
Ala Tyr Ala Pro Thr Ser Cys Ser Pro Thr Gln His Thr Glu Ala Phe
305                 310                 315                 320
Val Val Phe Tyr Phe Pro Leu Thr His Cys Gly Thr Thr Met Gln Val
                325                 330                 335
Ala Gly Asp Gln Leu Ile Tyr Glu Asn Trp Leu Val Ser Gly Ile His
                340                 345                 350
Ile Gln Lys Gly Pro Gln Gly Ser Ile Thr Arg Asp Ser Thr Phe Gln
                355                 360                 365
Leu His Val Arg Cys Val Phe Asn Ala Ser Asp Phe Leu Pro Ile Gln
    370                 375                 380
Ala Ser Ile Phe Pro Pro Pro Ser Pro Ala Pro Met Thr Gln Pro Gly
385                 390                 395                 400
Pro Leu Arg Leu Glu Leu Arg Ile Ala Lys Asp Glu Thr Cys Ser Ser
                405                 410                 415
Tyr Tyr Gly Glu Asp Asp Tyr Pro Ile Val Arg Leu Leu Arg Glu Pro
                420                 425                 430
Val His Val Glu Val Arg Leu Leu Gln Arg Thr Asp Pro Asn Leu Val
    435                 440                 445
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Leu Leu Leu His Gln Cys Trp Gly Ala Pro Ser Ala Asn Pro Phe Gln
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Gln Pro Gln Trp Pro Ile Leu Ser Asp Gly Cys Pro Phe Lys Gly Asp
465                 470                 475                 480
Ser Tyr Arg Thr Gln Met Val Ala Leu Asp Gly Ala Thr Pro Phe Gln
                485                 490                 495
Ser His Tyr Gln Arg Phe Thr Val Ala Thr Phe Ala Leu Leu Asp Ser
                500                 505                 510
Gly Ser Gln Arg Ala Leu Arg Gly Leu Val Tyr Leu Phe Cys Ser Thr
                515                 520                 525
Ser Ala Cys His Thr Ser Gly Leu Glu Thr Cys Ser Thr Ala Cys Ser
    530                 535                 540
Thr Gly Thr Thr Arg Gln Arg Arg Ser Ser Gly His Arg Asn Asp Thr
545                 550                 555                 560
Ala Arg Pro Gln Asp Ile Val Ser Ser Pro Gly Pro Val Gly Phe Glu
                565                 570                 575
Asp Ser Tyr Gly Gln Glu Pro Thr Leu Gly Pro Thr Asp Ser Asn Gly
                580                 585                 590
Asn Ser Ser Leu Arg Pro Leu Leu Trp Ala Val Leu Leu Leu Pro Ala
                595                 600                 605
Val Ala Leu Val Leu Gly Phe Gly Val Phe Val Gly Leu Ser Gln Thr
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Trp Ala Gln Lys Leu Trp Glu Ser Asn Arg Gln
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111, 123, 132, 141, 144, 147, 153, 156, 159, 162, 168, 171,
174, 183, 186, 198, 204, 213, 225, 243, 246, 249, 252
<223> n = A,T,C or G

<221> misc_feature
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825, 837, 843, 852, 855, 858, 861, 864, 876, 879, 882, 888,
894, 897, 900, 912, 915, 921, 924, 927, 930, 936, 939
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1656, 1659, 1662, 1665, 1671, 1680, 1683, 1686, 1689
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1788, 1791, 1794, 1797, 1800, 1806, 1809, 1812, 1815, 1818,
1821, 1824, 1827, 1830, 1833, 1836, 1839, 1842, 1848
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tgggcngtny tnytnytncc ngcngtngcn ytngtnytng gnttyggngt nttygtnggn 1860
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<220>
<223> Oligonucleotide primer ZC29717

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